

## RAW SEQUENCE LISTING

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Application Serial Number: 10/501,259  
Source: PCT  
Date Processed by STIC: 3-8-05

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PCT

## RAW SEQUENCE LISTING

DATE: 03/08/2005

PATENT APPLICATION: US/10/501,259

TIME: 07:56:34

Input Set : A:\61646 Sequence Listing.txt

Output Set: N:\CRF4\03082005\J501259.raw

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3 <110> APPLICANT: Shiozawa, Shunichi
5 <120> TITLE OF INVENTION: DNA structure and proteins responsible for the pathogenesis
6   of rheumatoid arthritis, diagnostic method of the disease,
7   diagnostic kit for detecting the disease,
8   treatment technique and curative medicine of the disease
10 <130> FILE REFERENCE: 61646 (70904)
12 <140> CURRENT APPLICATION NUMBER: 10/501,259
13 <141> CURRENT FILING DATE: 2004-07-09
15 <150> PRIOR APPLICATION NUMBER: PCT/JP03/00089
16 <151> PRIOR FILING DATE: 2003-01-08
18 <150> PRIOR APPLICATION NUMBER: JP 2002-005326
19 <151> PRIOR FILING DATE: 2002-01-11
21 <160> NUMBER OF SEQ ID NOS: 9
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 498
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
31 Met Thr Val Phe Leu Ser Phe Ala Phe Leu Ala Ala Ile Leu Thr His
32   1           5           10           15
33 Ile Gly Cys Ser Asn Gln Arg Arg Ser Pro Glu Asn Ser Gly Arg Arg
34   20           25           30
35 Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
36   35           40           45
37 Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
38   50           55           60
39 Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
40   65           70           75           80
41 Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
42   85           90           95
43 Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
44   100          105          110
45 Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
46   115          120          125
47 Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
48   130          135          140
49 Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
50 145          150          155          160
51 Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
52   165          170          175
53 Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
54   180          185          190

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55 Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
56      195      200      205
57 Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
58      210      215      220
59 Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
60 225      230      235      240
61 Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
62      245      250      255
63 Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
64      260      265      270
65 Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp
66      275      280      285
67 Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile
68      290      295      300
69 Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn
70 305      310      315      320
71 Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp
72      325      330      335
73 Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser
74      340      345      350
75 Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln
76      355      360      365
77 Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
78      370      375      380
79 Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
80 385      390      395      400
81 Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
82      405      410      415
83 Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
84      420      425      430
85 Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp
86      435      440      445
87 Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
88      450      455      460
89 Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
90 465      470      475      480
91 Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu
92      485      490      495
93 Asp Phe
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 1497
98 <212> TYPE: DNA
99 <213> ORGANISM: Homo sapiens
101 <400> SEQUENCE: 2
102 atgacagttt tcttttctt tgcctttctc gctgccattc tgactcacat aggggtgcagc 60
103 aatcagcgcc gaagtccaga aaacagtggg agaagatata accggattca acatgggcaa 120
104 tgtgcctaca ctttcattct tccagaacac gatggcaact gtcgtgagag tacgacagac 180
105 cagtacaaca caaacgctct gcagagagat gctccacacg tggaaccgga tttctcttcc 240
106 cagaaacttc aacatctgga acatgtgatg gaaaattata ctcagtggct gcaaaaactt 300

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107 gagaattaca ttgtggaaaa catgaagtcg gagatggccc agatacagca gaatgcagtt 360
108 cagaaccaca cggctacat gctggagata ggaaccagcc tcctctctca gactgcagag 420
109 cagaccagaa agctgacaga tgttgagacc caggtactaa atcaaacttc tcgacttgag 480
110 atacagctgc tggagaattc attatccacc tacaagctag agaagcaact tcttcaacag 540
111 acaaatgaaa tcttgaagat ccatgaaaaa aacagtttat tagaacataa aatcttagaa 600
112 atggaaggaa aacacaagga agagttggac accttaaagg aagagaaaaga gaaccttcaa 660
113 ggcttggtta ctgctcaaac atatataatc caggagctgg aaaagcaatt aaacagagct 720
114 accaccaaca acagtgtcct tcagaagcag caactggagc tgatggacac agtccacaac 780
115 cttgtcaatc tttgcactaa agaaggtggt ttactaaagg gaggaaaaag agaggaagag 840
116 aaaccattta gagactgtgc agatgtatat caagctgggt ttaataaaaag tggaatctac 900
117 actattttata ttaataatat gccagaaccc aaaaagggtg tttgcaatat ggatgtcaat 960
118 gggggagggtt ggactgtaat acaacatcgt gaagatggaa gtctagattt ccaaaggaggc 1020
119 tgggaaggaa ataaaatggg ttttggaaat ccctccggtg aatattggct ggggaatgag 1080
120 tttatttttg ccattaccag tcagaggcag tacatgctaa gaattgagtt aatggactgg 1140
121 gaagggaacc gagcctattc acagtatgac agattccaca taggaaatga aaagcaaac 1200
122 tataggttgt atttaaaagg tcacactggg acagcaggaa aacagagcag cctgatctta 1260
123 cacggtgctg atttcagcac taaagatgct gataatgaca actgtatgtg caaatgtgcc 1320
124 ctcatgttaa caggaggatg gtggtttgat gcttgtggcc cctccaatct aaatggaatg 1380
125 ttctatactg cgggacaaaa ccatggaaaa ctgaatggga taaagtggca ctacttcaaa 1440
126 gggcccagtt actccttacg ttccacaact atgatgattc gacctttaga ttttga 1497
129 <210> SEQ ID NO: 3
130 <211> LENGTH: 19
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthesized
136     oligonucleotide
138 <400> SEQUENCE: 3
139 gctggcagta caatgacag                                     19
142 <210> SEQ ID NO: 4
143 <211> LENGTH: 21
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthesized
149     oligonucleotide
151 <400> SEQUENCE: 4
152 tcaaaaatct aaaggtcgaa t                                     21
155 <210> SEQ ID NO: 5
156 <211> LENGTH: 19
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthesized
162     oligonucleotide
164 <400> SEQUENCE: 5
165 caaccttgtc aatctttgc                                     19
168 <210> SEQ ID NO: 6
169 <211> LENGTH: 20

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170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthesized
175     oligonucleotide
177 <400> SEQUENCE: 6
178 acaccttttt gggttctggc                20
181 <210> SEQ ID NO: 7
182 <211> LENGTH: 18
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthesized
188     oligonucleotide
190 <400> SEQUENCE: 7
191 ttgcgagag gcacggaa                18
194 <210> SEQ ID NO: 8
195 <211> LENGTH: 20
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthesized
201     oligonucleotide
203 <400> SEQUENCE: 8
204 tatatcttct cccactgttt                20
207 <210> SEQ ID NO: 9
208 <211> LENGTH: 27
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthesized
214     oligonucleotide
216 <400> SEQUENCE: 9
217 ttctctgctg ccattctgac tcacata        27

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**VERIFICATION SUMMARY**

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